

SEQUENCE LISTING

<110> Duprat, Fabrice
Lesage, Florian
Fink, Michel
Lazdunski, Michel

<120> FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

<130> 1201-CIP-DIV-00

<141> 2001-08-24

<150> 09/144,914

<151> 1998-09-01

<150> 08/749,816

<151> 1996-11-15

<150> 60/095,234

<151> 1998-08-04

<150> FR 96/01565

<151> 1996-02-08

<160> 24

<170> PatentIn Ver. 2.0

<210> 1

<211> 1894

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)..(1190)

<220>

<223> TWIK-1

<400> 1

```

gggcaggaag acggcgctgc ccggaggagc ggggcgggcg ggcgcgcggg ggagcgggcg 60
gcgggcggga gccaggcccg ggcgggggcg ggggcggcgg ggccagaaga ggcggcgggc 120
cgcgctccgg ccggtctgcg gcgttggcct tggctttggc tttggcggcg gcggtggaga 180
ag atg ctg cag tcc ctg gcc ggc agc tcg tgc gtg cgc ctg gtg gag 227
Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu
1 5 10 15
cgg cac cgc tcg gcc tgg tgc ttc ggc ttc ctg gtg ctg ggc tac ttg 275
Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu
20 25 30
ctc tac ctg gtc ttc ggc gca gtg gtc ttc tcc tcg gtg gag ctg ccc 323
Leu Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro
35 40 45

```

tat	gag	gac	ctg	ctg	cgc	cag	gag	ctg	cgc	aag	ctg	aag	cga	cgc	ttc	371
Tyr	Glu	Asp	Leu	Leu	Arg	Gln	Glu	Leu	Arg	Lys	Leu	Lys	Arg	Arg	Phe	
	50						55					60				
ttg	gag	gag	cac	gag	tgc	ctg	tct	gag	cag	cag	ctg	gag	cag	ttc	ctg	419
Leu	Glu	Glu	His	Glu	Cys	Leu	Ser	Glu	Gln	Gln	Leu	Glu	Gln	Phe	Leu	
	65					70					75					
ggc	cgg	gtg	ctg	gag	gcc	agc	aac	tac	ggc	gtg	tcg	gtg	ctc	agc	aac	467
Gly	Arg	Val	Leu	Glu	Ala	Ser	Asn	Tyr	Gly	Val	Ser	Val	Leu	Ser	Asn	
	80				85					90					95	
gcc	tcg	ggc	aac	tgg	aac	tgg	gac	ttc	acc	tcc	gcg	ctc	ttc	ttc	gcc	515
Ala	Ser	Gly	Asn	Trp	Asn	Trp	Asp	Phe	Thr	Ser	Ala	Leu	Phe	Phe	Ala	
				100					105					110		
agc	acc	gtg	ctc	tcc	acc	aca	ggt	tat	ggc	cac	acc	gtg	ccc	ttg	tca	563
Ser	Thr	Val	Leu	Ser	Thr	Thr	Gly	Tyr	Gly	His	Thr	Val	Pro	Leu	Ser	
			115					120					125			
gat	gga	ggt	aag	gcc	ttc	tgc	atc	atc	tac	tcc	gtc	att	ggc	att	ccc	611
Asp	Gly	Gly	Lys	Ala	Phe	Cys	Ile	Ile	Tyr	Ser	Val	Ile	Gly	Ile	Pro	
		130					135					140				
ttc	acc	ctc	ctg	ttc	ctg	acg	gct	gtg	gtc	cag	cgc	atc	acc	gtg	cac	659
Phe	Thr	Leu	Leu	Phe	Leu	Thr	Ala	Val	Val	Gln	Arg	Ile	Thr	Val	His	
	145					150					155					
gtc	acc	cgc	agg	ccg	gtc	ctc	tac	ttc	cac	atc	cgc	tgg	ggc	ttc	tcc	707
Val	Thr	Arg	Arg	Pro	Val	Leu	Tyr	Phe	His	Ile	Arg	Trp	Gly	Phe	Ser	
	160				165					170					175	
aag	cag	gtg	gtg	gcc	atc	gtc	cat	gcc	gtg	ctc	ctt	ggg	ttt	gtc	act	755
Lys	Gln	Val	Val	Ala	Ile	Val	His	Ala	Val	Leu	Leu	Gly	Phe	Val	Thr	
				180					185					190		
gtg	tcc	tgc	ttc	ttc	ttc	atc	ccg	gcc	gct	gtc	ttc	tca	gtc	ctg	gag	803
Val	Ser	Cys	Phe	Phe	Phe	Ile	Pro	Ala	Ala	Val	Phe	Ser	Val	Leu	Glu	
			195					200					205			
gat	gac	tgg	aac	ttc	ctg	gaa	tcc	ttt	tat	ttt	tgt	ttt	att	tcc	ctg	851
Asp	Asp	Trp	Asn	Phe	Leu	Glu	Ser	Phe	Tyr	Phe	Cys	Phe	Ile	Ser	Leu	
		210					215					220				
agc	acc	att	ggc	ctg	ggg	gat	tat	gtg	cct	ggg	gaa	ggc	tac	aat	caa	899
Ser	Thr	Ile	Gly	Leu	Gly	Asp	Tyr	Val	Pro	Gly	Glu	Gly	Tyr	Asn	Gln	
		225				230					235					
aaa	ttc	aga	gag	ctc	tat	aag	att	ggg	atc	acg	tgt	tac	ctg	cta	ctt	947
Lys	Phe	Arg	Glu	Leu	Tyr	Lys	Ile	Gly	Ile	Thr	Cys	Tyr	Leu	Leu	Leu	
	240				245					250					255	
ggc	ctt	att	gcc	atg	ttg	gta	gtt	ctg	gaa	acc	ttc	tgt	gaa	ctc	cat	995
Gly	Leu	Ile	Ala	Met	Leu	Val	Val	Leu	Glu	Thr	Phe	Cys	Glu	Leu	His	
				260					265					270		
gag	ctg	aaa	aaa	ttc	aga	aaa	atg	ttc	tat	gtg	aag	aag	gac	aag	gac	1043
Glu	Leu	Lys	Lys	Phe	Arg	Lys	Met	Phe	Tyr	Val	Lys	Lys	Asp	Lys	Asp	
		275						280					285			
gag	gat	cag	gtg	cac	atc	ata	gag	cat	gac	caa	ctg	tcc	ttc	tcc	tcg	1091

Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser
 290 295 300

atc aca gac cag gca gct ggc atg aaa gag gac cag aag caa aat gag 1139
 Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu
 305 310 315

cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac 1187
 Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn
 320 325 330 335

cat tgagcgtagg atttggtgca ttatgctaga gcaccagggg caggggtgcaa 1240
 His

ggaagaggct taagtatggt catttttatc agaatgcaaa agcgaaaatt atgtcacttt 1300

aagaaatagc tactgtttgc aatgtcttat taaaaaacia caaaaaaaga cacatggaac 1360

aaagaagctg tgaccccgagc aggatgtcta atatgtgagg aatgagatg tccacctaaa 1420

attcatatgt gacaaaatta tctcgacctt acataggagg agaatacttg aagcagtatg 1480

ctgctgtggt tagaagcaga ttttatactt ttaactggaa actttggggg ttgcatttag 1540

atcatttagc tgatggctaa atagcaaaat ttatathtag aagcaaaaaa aaaaagcata 1600

gagatgtggt ttataaatag gtttatgtgt actggtttgc atgtaccac ccaaaatgat 1660

tatttttga gaatctaagt caaactcact atttataatg cataggtaac cattaactat 1720

gtacatataa agtataaata tgtttatatt ctgtacatat ggttttaggtc accagatcct 1780

agtgtagttc tgaaactaag actatagata ttttgtttct tttgatttct ctttatacta 1840

aagaatccag agttgctaca ataaaataag ggaataata aaaaaaaaaa aaaa 1894

<210> 2

<211> 336

<212> PRT

<213> Homo sapiens

<220>

<223> TWIK-1

<400> 2

Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu Arg
 1 5 10 15

His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
 20 25 30

Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
 35 40 45

Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
 50 55 60

Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
 65 70 75 80

[illegible]

tgccctgcgc	ggatagcggc	gagcgcagcc	atgccccagg	ccgcctccgg	ggcagcagca	60										
gcggcgggccg	gggccgatgc	gcgggccggg	ggcgccgggg	ggccggcggc	ggccccgggcg	120										
ggacg	atg	aag	cgg	cag	aac	gtg	cgc	acg	ctg	gcg	ctc	atc	gtg	tgc	acc	170
	Met	Lys	Arg	Gln	Asn	Val	Arg	Thr	Leu	Ala	Leu	Ile	Val	Cys	Thr	
	1				5					10					15	
ttc	acc	tac	ctg	ctg	gtg	ggc	gcc	gcg	gtc	ttc	gac	gcg	ctg	gag	tcg	218
Phe	Thr	Tyr	Leu	Leu	Val	Gly	Ala	Ala	Val	Phe	Asp	Ala	Leu	Glu	Ser	
				20					25					30		
gag	ccc	gag	ctg	atc	gag	cgg	cag	cgg	ctg	gag	ctg	cgg	cag	cag	gag	266
Glu	Pro	Glu	Leu	Ile	Glu	Arg	Gln	Arg	Leu	Glu	Leu	Arg	Gln	Gln	Glu	
			35					40					45			
ctg	cgg	gcg	cgc	tac	aac	ctc	agc	cag	ggc	ggc	tac	gag	gag	ctg	gag	314
Leu	Arg	Ala	Arg	Tyr	Asn	Leu	Ser	Gln	Gly	Gly	Tyr	Glu	Glu	Leu	Glu	
		50					55					60				
cgc	gtc	gtg	ctg	cgc	ctc	aag	ccg	cac	aag	gcc	ggc	gtg	cag	tgg	cgc	362
Arg	Val	Val	Leu	Arg	Leu	Lys	Pro	His	Lys	Ala	Gly	Val	Gln	Trp	Arg	
	65					70					75					
ttc	gcc	ggc	tcc	ttc	tac	ttc	gcc	atc	acc	gtc	atc	acc	acc	atc	ggc	410
Phe	Ala	Gly	Ser	Phe	Tyr	Phe	Ala	Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	
80					85					90					95	
tac	ggg	cac	gcg	gca	ccc	agc	acg	gat	ggc	ggc	aag	gtg	ttc	tgc	atg	458
Tyr	Gly	His	Ala	Ala	Pro	Ser	Thr	Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	
				100					105					110		
ttc	tac	gcg	ctg	ctg	ggc	atc	ccg	ctc	acg	ctc	gtc	atg	ttc	cag	agc	506
Phe	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Thr	Leu	Val	Met	Phe	Gln	Ser	
			115					120					125			
ctg	ggc	gag	cgc	atc	aac	acc	ttg	gtg	agg	tac	ctg	ctg	cac	cgc	gcc	554
Leu	Gly	Glu	Arg	Ile	Asn	Thr	Leu	Val	Arg	Tyr	Leu	Leu	His	Arg	Ala	
		130					135					140				
aag	aag	ggg	ctg	ggc	atg	cgg	cgc	gcc	gac	gtg	tcc	atg	gcc	aac	atg	602
Lys	Lys	Gly	Leu	Gly	Met	Arg	Arg	Ala	Asp	Val	Ser	Met	Ala	Asn	Met	
	145					150					155					
gtg	ctc	atc	ggc	ttc	ttc	tcg	tgc	atc	agc	acg	ctg	tgc	atc	ggc	gcc	650
Val	Leu	Ile	Gly	Phe	Phe	Ser	Cys	Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	
160					165					170					175	
gcc	gcc	ttc	tcc	cac	tac	gag	cac	tgg	acc	ttc	ttc	cag	gcc	tac	tac	698
Ala	Ala	Phe	Ser	His	Tyr	Glu	His	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	
				180				185						190		
tac	tgc	ttc	atc	acc	ctc	acc	acc	atc	ggc	ttc	ggc	gac	tac	gtg	gcg	746
Tyr	Cys	Phe	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	
			1													

agc Ser	ttc Phe	gtc Val	tac Tyr	atc Ile	ctt Leu	acg Thr	ggc Gly	ctc Leu	acg Thr	gtc Val	atc Ile	ggc Gly	gcc Ala	ttc Phe	ctc Leu	842	
aac Asn	ctc Leu	gtg Val	gtg Val	ctg Leu	cgc Arg	ttc Phe	atg Met	acc Thr	atg Met	aac Asn	gcc Ala	gag Glu	gac Asp	gag Glu	aag Lys	890	
cgc Arg	gac Asp	gcc Ala	gag Glu	cac His	cgc Arg	gcg Ala	ctg Leu	ctc Leu	acg Thr	cgc Arg	aac Asn	ggg Gly	cag Gln	gcg Ala	ggc Gly	938	
ggc Gly	ggc Gly	gga Gly	ggg Gly	ggt Gly	ggc Gly	agc Ser	gcg Ala	cac His	act Thr	acg Thr	gac Asp	acc Thr	gcc Ala	tca Ser	tcc Ser	986	
acg Thr	gcg Ala	gca Ala	gcg Ala	ggc Gly	ggc Gly	ggc Gly	ggc Gly	ttc Phe	cgc Arg	aac Asn	gtc Val	tac Tyr	gcg Ala	gag Glu	gtg Val	1034	
ctg Leu	cac His	ttc Phe	cag Gln	tcc Ser	atg Met	tgc Cys	tcg Ser	tgc Cys	ctg Leu	tgg Trp	tac Tyr	aag Lys	agc Ser	cgc Arg	gag Glu	1082	
aag Lys	ctg Leu	cag Gln	tac Tyr	tcc Ser	atc Ile	ccc Pro	atg Met	atc Ile	atc Ile	ccg Pro	cgg Arg	gac Asp	ctc Leu	tcc Ser	acg Thr	1130	
tcc Ser	gac Asp	acg Thr	tgc Cys	gtg Val	gag Glu	cag Gln	agc Ser	cac His	tcg Ser	tcg Ser	ccg Pro	gga Gly	ggg Gly	ggc Gly	ggc Gly	1178	
cgc Arg	tac Tyr	agc Ser	gac Asp	acg Thr	ccc Pro	tcg Ser	cga Arg	cgc Arg	tgc Cys	ctg Leu	tgc Cys	agc Ser	ggg Gly	gcg Ala	cca Pro	1226	
cgc Arg	tcc Ser	gcc Ala	atc Ile	agc Ser	tcg Ser	gtg Val	tcc Ser	acg Thr	ggg Gly	ctg Leu	cac His	agc Ser	ctg Leu	tcc Ser	acc Thr	1274	
ttc Phe	cgc Arg	ggc Gly	ctc Leu	atg Met	aag Lys	cgc Arg	agg Arg	agc Ser	tcc Ser	gtg Val	tgactgcccc				gagggacctg		1327
gagcacctgg		gggcgcgggc		gggggacccc		tgctgggagg		ccaggagact		gcccctgctg						1387	
ccttctgccc		agtgggaccc		cgcacaacat		ccctcaccac		tctccccag		cacccecatc						1447	
tccgactgtg		cctgcttgca		ccagccggca		ggaggccggg		ctctgaggac		ccctggggcc						1507	
cccatcggag		ccctgcaaata		tccgagaaat		gtgaaacttg		gtggggtcag		ggaggaaagg						1567	
cagaagctgg		gagcctccct		tccctttgaa		aatctaagaa		gctcccagtc		ctcagagacc						1627	
ctgctgggtac		cacaccccac		cttcggagggg		gacttcatgt		tccgtgtaag		tttgcatctc						1687	
tatttatacc		tctgtcctgc		taggtctccc		accttccctt		ggttccaaaa		gccagggtgt						1747	
ctatgtccaa		gtcaccacct		ctcagcccca		ctccccttcc		tcatccccag		ctgtgtctcc						1807	
caacctccct		tcgtgttggt		ttgcatggct		ttgcagttat		ggagaaaqtg		qaaacccagc						1867	

agtccctaaa gctggtcccc agaaagcagg acagaaagaa ggagggacag gcaggcagca 1927
 ggaggggga gctgggagggc aggaggcagc ggctgtcag tctgcagaat ggtcgactg 1987
 gaggttcaag ctaactggcc tccagccaca ttctcatagc aggtaggact tcagccttcc 2047
 agacactgcc cttagaatct ggaacagaag acttcagact caccataatt gctgataatt 2107
 acccactctt aaatttgtcg agtgattttt agcctctgaa aactctatgc tggccactga 2167
 ttcctttgag tctcacaaaa ccctacttag gtcacagggc caggagtctt cactcccatt 2227
 ttacagatga acctgtattc ccaacacttt tggaggctga ggttggagga ttgcttgagc 2287
 ccaggaattc gagaccagcc taggtgacat agtgagaccc catctctaca aaaaataaaa 2347
 aattaaccag gtgtggtggc acgtgcctgg gagtcccagc gaattgggag gctgaggtgg 2407
 gaggattgtt tgagcctggg aggtcgaggc tgtagtgagc cctgattgca cactgtact 2467
 ccagcctggg tgacagggca agaccctgtc tcaaaaaaaaa aaaaaaa 2514

<210> 4
 <211> 394
 <212> PRT
 <213> Homo sapiens

<220>
 <223> TASK

<400> 4

Met	Lys	Arg	Gln	Asn	Val	Arg	Thr	Leu	Ala	Leu	Ile	Val	Cys	Thr	Phe
1				5					10					15	
Thr	Tyr	Leu	Leu	Val	Gly	Ala	Ala	Val	Phe	Asp	Ala	Leu	Glu	Ser	Glu
			20					25					30		
Pro	Glu	Leu	Ile	Glu	Arg	Gln	Arg	Leu	Glu	Leu	Arg	Gln	Gln	Glu	Leu
		35					40					45			
Arg	Ala	Arg	Tyr	Asn	Leu	Ser	Gln	Gly	Gly	Tyr	Glu	Glu	Leu	Glu	Arg
		50				55					60				
Val	Val	Leu	Arg	Leu	Lys	Pro	His	Lys	Ala	Gly	Val	Gln	Trp	Arg	Phe
65					70					75					80
Ala	Gly	Ser	Phe	Tyr	Phe	Ala	Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr
			85					90						95	
Gly	His	Ala	Ala	Pro	Ser	Thr	Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	Phe
		100						105					110		
Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Thr	Leu	Val	Met	Phe	Gln	Ser	Leu
		115					120					125			
Gly	Glu	Arg	Ile	Asn	Thr	Leu	Val	Arg	Tyr	Leu	Leu	His	Arg	Ala	Lys
	130					135					140				
Lys	Gly	Leu	Gly	Met	Arg	Arg	Ala	Asp	Val	Ser	Met	Ala	Asn	Met	Val

145		150		155		160
Leu Ile Gly Phe	Phe Ser Cys Ile Ser Thr	Leu Cys Ile Gly	Ala Ala			
	165		170		175	
Ala Phe Ser His	Tyr Glu His Trp Thr	Phe Phe Gln Ala	Tyr Tyr Tyr			
	180		185		190	
Cys Phe Ile Thr	Leu Thr Thr Ile	Gly Phe Gly Asp	Tyr Val Ala Leu			
	195		200		205	
Gln Lys Asp Gln	Ala Leu Gln Thr	Gln Pro Gln Tyr	Val Ala Phe Ser			
	210		215		220	
Phe Val Tyr Ile	Leu Thr Gly Leu	Thr Val Ile Gly	Ala Phe Leu Asn			
	225		230		235	
Leu Val Val Leu	Arg Phe Met Thr	Met Asn Ala Glu	Asp Glu Lys Arg			
	245		250		255	
Asp Ala Glu His	Arg Ala Leu Leu	Thr Arg Asn Gly	Gln Ala Gly Gly			
	260		265		270	
Gly Gly Gly Gly	Gly Ser Ala His	Thr Thr Asp Thr	Ala Ser Ser Thr			
	275		280		285	
Ala Ala Ala Gly	Gly Gly Gly Phe	Arg Asn Val Tyr	Ala Glu Val Leu			
	290		295		300	
His Phe Gln Ser	Met Cys Ser Cys	Leu Trp Tyr Lys	Ser Arg Glu Lys			
	305		310		315	
Leu Gln Tyr Ser	Ile Pro Met Ile	Ile Pro Arg Asp	Leu Ser Thr Ser			
	325		330		335	
Asp Thr Cys Val	Glu Gln Ser His	Ser Ser Pro Gly	Gly Gly Gly Arg			
	340		345		350	
Tyr Ser Asp Thr	Pro Ser Arg Arg	Cys Leu Cys Ser	Gly Ala Pro Arg			
	355		360		365	
Ser Ala Ile Ser	Ser Val Ser Thr	Gly Leu His Ser	Leu Ser Thr Phe			
	370		375		380	
Arg Gly Leu Met	Lys Arg Arg Ser	Ser Val				
	385		390			

<210> 5
 <211> 405
 <212> PRT
 <213> Murine

<220>
 <223> TASK

<400> 5
 Glu Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu
 1 5 10 15

Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met

	20						25						30					
Ile	Glu	Arg	Gln	Arg	Leu	Glu	Leu	Arg	Gln	Leu	Glu	Leu	Arg	Ala	Arg			
		35					40					45						
Tyr	Asn	Leu	Ser	Glu	Gly	Gly	Tyr	Glu	Glu	Leu	Glu	Arg	Val	Val	Leu			
	50					55					60							
Arg	Leu	Lys	Pro	His	Lys	Ala	Gly	Val	Gln	Trp	Arg	Phe	Ala	Gly	Ser			
	65				70					75					80			
Phe	Tyr	Phe	Ala	Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr	Gly	His	Ala			
				85					90					95				
Ala	Pro	Ser	Thr	Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	Phe	Tyr	Ala	Leu			
			100					105					110					
Leu	Gly	Ile	Pro	Leu	Thr	Leu	Ile	Met	Phe	Gln	Ser	Leu	Gly	Glu	Arg			
		115					120					125						
Ile	Asn	Thr	Phe	Val	Arg	Tyr	Leu	Leu	His	Arg	Ala	Lys	Arg	Gly	Leu			
	130					135					140							
Gly	Met	Arg	His	Ala	Glu	Val	Ser	Met	Ala	Asn	Met	Val	Leu	Ile	Gly			
145					150					155					160			
Phe	Val	Ser	Cys	Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	Ala	Ala	Phe	Ser			
				165					170					175				
Tyr	Tyr	Glu	Arg	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr	Cys	Phe	Ile			
			180					185					190					
Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	Leu	Gln	Lys	Asp			
		195					200					205						
Gln	Ala	Leu	Gln	Thr	Gln	Pro	Gln	Tyr	Val	Ala	Phe	Ser	Phe	Val	Tyr			
	210					215					220							
Ile	Leu	Thr	Gly	Leu	Thr	Val	Ile	Gly	Ala	Phe	Leu	Asn	Leu	Val	Val			
225					230					235					240			
Leu	Arg	Phe	Met	Thr	Met	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Asp	Ala	Glu			
				245					250					255				
His	Arg	Ala	Leu	Leu	Thr	His	Asn	Gly	Gln	Ala	Val	Gly	Leu	Gly	Gly			
			260					265					270					
Leu	Ser	Cys	Leu	Ser	Gly	Ser	Leu	Gly	Asp	Val	Arg	Pro	Arg	Asp	Pro			
		275					280					285						
Val	Thr	Cys	Ala	Ala	Ala	Ala	Gly	Gly	Val	Gly	Val	Gly	Val	Gly	Gly			
	290					295					300							
Ser	Gly	Phe	Arg	Asn	Val	Tyr	Ala	Glu	Val	Leu	His	Phe	Gln	Ser	Met			
305					310					315					320			
Cys	Ser	Cys	Leu	Trp	Tyr	Lys	Ser	Arg	Glu	Lys	Leu	Gln	Tyr	Ser	Ile			
				325					330					335				
Pro	Met	Ile	Ile	Pro	Arg	Asp	Leu	Ser	Thr	Ser	Asp	Thr	Cys	Val	Glu			
			340					345					350					

His Ser His Ser Ser Pro Gly Gly Gly Gly Arg Tyr Ser Asp Thr Pro
 355 360 365

Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser Ala Ile Ser Ser
 370 375 380

Val Ser Thr Gly Leu His Ser Leu Ala Ala Phe Arg Gly Leu Met Lys
 385 390 395 400

Arg Arg Ser Ser Val
 405

<210> 6
 <211> 347
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: TWIK-1 homolog

<400> 6
 Met Tyr Thr Asp Glu Gly Glu Tyr Ser Gly Asp Thr Asp His Gly Gly
 1 5 10 15

Ser Thr Met Gln Lys Met Ser Pro Asn Thr Arg Gln Asn Phe Arg Gln
 20 25 30

Asn Val Asn Val Val Val Cys Leu Ser Ala Ala Ile Thr Leu Leu Val
 35 40 45

Phe Asn Leu Ile Gly Ala Gly Ile Phe Tyr Leu Ala Glu Thr Gln Asn
 50 55 60

Ser Ser Glu Ser Leu Asn Glu Asn Ser Glu Val Ser Lys Cys Leu His
 65 70 75 80

Asn Leu Pro Ile Gly Gly Lys Ile Thr Ala Glu Met Lys Ser Lys Leu
 85 90 95

Gly Lys Cys Leu Thr Lys Ser Ser Arg Ile Asp Gly Phe Gly Lys Ala
 100 105 110

Ile Phe Phe Ser Trp Thr Leu Tyr Ser Thr Val Gly Tyr Gly Ser Leu
 115 120 125

Tyr Pro His Ser Thr Leu Gly Arg Tyr Leu Thr Ile Phe Tyr Ser Leu
 130 135 140

Leu Met Ile Pro Val Phe Ile Ala Phe Lys Phe Glu Phe Gly Thr Phe
 145 150 155 160

Leu Ala His Phe Leu Val Val Val Ser Asn Arg Thr Arg Leu Ala Val
 165 170 175

Lys Lys Ala Tyr Tyr Lys Leu Ser Gln Asn Pro Glu Asn Ala Glu Thr
 180 185 190

Pro Ser Asn Ser Leu Gln His Asp Tyr Leu Ile Phe Leu Ser Ser Leu
 195 200 205

Leu Leu Cys Ser Ile Ser Leu Leu Ser Ser Ser Ala Leu Phe Ser Ser
210 215 220

Ile Glu Asn Ile Ser Tyr Leu Ser Ser Val Tyr Phe Gly Ile Ile Thr
225 230 235 240

Met Phe Leu Ile Gly Ile Gly Asp Ile Val Pro Thr Asn Leu Val Trp
245 250 255

Phe Ser Gly Tyr Cys Met Leu Phe Leu Ile Ser Asp Val Leu Ser Asn
260 265 270

Gln Ile Phe Tyr Phe Cys Gln Ala Arg Val Arg Tyr Phe Phe His Ile
275 280 285

Leu Ala Arg Lys Ile Leu Leu Leu Arg Glu Glu Asp Asp Gly Phe Gln
290 295 300

Leu Glu Thr Thr Val Ser Leu Gln His Ile Pro Ile Ile Asn Ser Gln
305 310 315 320

Cys Met Pro Ser Leu Val Leu Asp Cys Glu Lys Glu Glu Leu Asp Asn
325 330 335

Asp Glu Lys Leu Ile Ser Ser Leu Thr Ser Thr
340 345

<210> 7

<211> 383

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: TWIK-1 homolog

<400> 7

Met Thr Val Ser Met Glu Glu Asn Ser Lys Ile Gln Met Leu Ser Ala
1 5 10 15

Thr Ser Lys Asp Lys Lys Val Ala Thr Asp Arg Ser Leu Leu Asn Lys
20 25 30

Tyr His Leu Gly Pro Leu Ala Leu His Thr Gly Leu Val Leu Ser Cys
35 40 45

Val Thr Tyr Ala Leu Gly Gly Ala Tyr Leu Phe Leu Ser Ile Glu His
50 55 60

Pro Glu Glu Leu Lys Arg Arg Glu Lys Ala Ile Arg Glu Phe Gln Asp
65 70 75 80

Leu Lys Gln Gln Phe Met Gly Asn Ile Thr Ser Gly Ile Glu Asn Ser
85 90 95

Glu Gln Ser Ile Glu Ile Tyr Thr Lys Lys Leu Ile Leu Met Leu Glu
100 105 110

Asp Ala His Asn Ala His Ala Phe Glu Tyr Phe Phe Leu Asn His Glu
115 120 125

Lys	Pro	Arg	Leu	Ser	Phe	Ser	Ser	Lys	Pro	Thr	Val	Leu	Ala	Ser	Arg	
			20				25						30			
Val	Glu	Ser	Asp	Ser	Ala	Ile	Asn	Val	Met	Lys	Trp	Lys	Thr	Val	Ser	
			35				40						45			
Thr	Ile	Phe	Leu	Val	Val	Val	Leu	Tyr	Leu	Ile	Ile	Gly	Ala	Ala	Val	
			50				55						60			
Phe	Lys	Ala	Leu	Glu	Gln	Pro	Gln	Glu	Ile	Ser	Gln	Arg	Thr	Thr	Ile	
			65				70						75	80		
Val	Ile	Gln	Lys	Gln	Thr	Phe	Ile	Ala	Gln	His	Ala	Cys	Val	Asn	Ser	
			85						90						95	
Thr	Glu	Leu	Asp	Glu	Leu	Ile	Gln	Gln	Ile	Val	Ala	Ala	Ile	Asn	Ala	
			100						105						110	
Gly	Ile	Ile	Pro	Leu	Gly	Asn	Ser	Ser	Asn	Gln	Val	Ser	His	Trp	Asp	
			115						120						125	
Leu	Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly	
			130						135						140	
Phe	Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile	
			145						150						155	160
Ile	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Glu	Gly	Phe	Leu	Leu	Ala	Gly	
			165						170						175	
Val	Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val	
			180						185						190	
Glu	Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	Ile	
			195						200						205	
Ile	Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	Ala	
			210						215						220	
Leu	Pro	Ala	Val	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	Asp	
			225						230						235	240
Ala	Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	
			245						250						255	
Tyr	Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	Pro	
			260						265						270	
Val	Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	Val	
			275						280						285	
Leu	Ser	Met	Ile	Gly	Asp	Trp	Leu	Arg	Val	Ile	Ser	Lys	Lys	Thr	Lys	
			290						295						300	
Glu	Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	Asn	
			305						310						315	320
Val	Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	Ile	
			325						330						335	

Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala
340 345 350

Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Met Arg Thr
355 360 365

Cys Leu
370

<210> 9
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P1

<400> 9
Phe Thr Ser Ala Leu Phe Phe Ala Ser Thr Val Leu Ser Thr Thr Gly
1 5 10 15

Tyr Gly His Thr Val Pro Leu Ser Asp Gly Gly
20 25

<210> 10
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P2

<400> 10
Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser Thr Ile Gly
1 5 10 15

Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn
20 25

<210> 11
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> TOK-1 P2

<400> 11
Tyr Phe Asn Cys Ile Tyr Phe Cys Phe Leu Cys Leu Leu Thr Ile Gly
1 5 10 15

Tyr Gly Asp Tyr Ala Pro Arg Thr Gly Ala Gly
20 25

<210> 12
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> TOK-1 P1

<400> 12
Tyr Gly Asn Ala Leu Tyr Phe Cys Thr Val Ser Leu Leu Thr Val Gly
1 5 10 15
Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala
20 25

<210> 13
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> Slo

<400> 13
Tyr Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly
1 5 10 15
Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly
20 25

<210> 14
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> Shaker

<400> 14
Ile Pro Asp Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly
1 5 10 15
Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly
20 25

<210> 15
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shab

<400> 15
Ile Pro Glu Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Ile Cys Pro Thr Thr Ala Leu Gly
20 25

<210> 16
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shal

<400> 16
Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly
1 5 10 15

Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly
20 25

<210> 17
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shaw

<400> 17
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly
20 25

<210> 18

<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> KAT1

<400> 18
Tyr Val Thr Ala Leu Tyr Trp Ser Ile Thr Thr Leu Thr Thr Thr Gly
1 5 10 15

Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu
20 25

<210> 19
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> AKT1

<400> 19
Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu
20 25

<210> 20
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> eag

<400> 20
Tyr Val Thr Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly
1 5 10 15

Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu
20 25

<210> 21
<211> 27

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> ROMK1

<400> 21
Met Thr Ser Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly
1 5 10 15

Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala
20 25

<210> 22
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> IRK1

<400> 22
Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly
1 5 10 15

Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro
20 25

<210> 23
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> GIRK1

<400> 23
Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly
1 5 10 15

Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro
20 25

<210> 24
<211> 48
<212> DNA

